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TECH CENTER 1600/2900

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/671,050

DATE: 06/21/2001
 TIME: 17:53:52

Input Set : A:\lex46 SEQLIST.TXT
 Output Set: N:\CRF3\06212001\I671050.raw

ENTERED

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4 <110> APPLICANT: Donoho, Gregory
5     Turner, C. Alexander Jr.
6     Nehls, Michael
7     Friedrich, Glenn
8     Zambrowicz, Brian
9     Sands, Arthur T.
11 <120> TITLE OF INVENTION: Novel Human Kinase Proteins and
12     Polynucleotides Encoding the Same
14 <130> FILE REFERENCE: LEX-0046-USA
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/671,050
C--> 16 <141> CURRENT FILING DATE: 2001-06-11
16 <150> PRIOR APPLICATION NUMBER: US 60/156,511
17 <151> PRIOR FILING DATE: 1999-09-28
19 <160> NUMBER OF SEQ ID NOS: 13
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31 gatcctgttg ttaagaaaat agcactaaga gaaatacgta tgttgaagca attaaaacat      180
32 ccaaattctg tgaacctcat cgagggtgttc aggagaaaaa ggaaaatgca tttagttttt      240
33 gaatactgtg atcatacact tttaaatgag ctggaaagaa acccaaatgg agttgctgat      300
34 ggagtgatca aaagcgtatt atggcaaaca cttcaagctc ttaatttctg tcatatacat      360
35 aactgtattc acagagatat aaaacctgaa aatattctaa taactaagca aggaataatc      420
36 aagatttggt acttcgggtt tgacaaaatt ctgagttgga cttcatcttt ctctggtgcc      480
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48 Val Val Phe Lys Cys Arg Asn Lys Thr Ser Gly Gln Val Val Ala Val
49          20          25          30
50 Lys Lys Phe Val Glu Ser Glu Asp Pro Val Val Lys Lys Ile Ala
51          35          40          45
52 Leu Arg Glu Ile Arg Met Leu Lys Gln Leu Lys His Pro Asn Leu Val
53          50          55          60
54 Asn Leu Ile Glu Val Phe Arg Arg Lys Arg Lys Met His Leu Val Phe
55 65          70          75          80
56 Glu Tyr Cys Asp His Thr Leu Leu Asn Glu Leu Glu Arg Asn Pro Asn
57          85          90          95

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58 Gly Val Ala Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln
59                               100 105 110
60 Ala Leu Asn Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys
61                               115 120 125
62 Pro Glu Asn Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp
63                               130 135 140
64 Phe Gly Phe Ala Gln Ile Leu Ser Trp Thr Ser Ser Phe Ser Gly Ala
65 145                               150 155 160
66 Ser Leu Ile Gly Leu Ile Val Asp Leu Leu Asn Ser Phe Ser Ala Asn
67                               165 170 175
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69                               180 185
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79 gatcctgttg ttaagaaaat agcactaaga gaaatacgta tgttgaagca attaaaacat 180
80 ccaaatcttg tgaacctcat cgagggtgtt aggagaaaaa ggaaatgca tttagttttt 240
81 gaatactgtg atcatatact tttaaatgag ctggaaagaa acccaaatg agttgctgat 300
82 ggagtgatca aaagcgtatt atggcaaaca cttcaagctc ttaatttctg tcatatacat 360
83 aactgtattc acagagatat aaaacctgaa aatattctaa taactaagca aggaataatc 420
84 aagatttggt acttcgggtt tgcacaaatt ctgattccag gagatgccta caccgattat 480
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87 tggcctggaa aatcagatgt ggaccaactt tatctgataa tcagaacact agtagagacg 660
88 gggtttcgcc atggttgacca ggctgggtct gaactcttga cgtcaagtga tccacctgcc 720
89 gtagcctctc aaagtgtctg aattacagga aaattaatcc caagacatca atcaatcttt 780
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93 tttcaagagg ccaaatttaa aagaaaagca cgtaatgaag gaagaaacag aagacgcaa 1020
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106 Lys Lys Phe Val Glu Ser Glu Asp Asp Pro Val Val Lys Lys Ile Ala
107 35 40 45
108 Leu Arg Glu Ile Arg Met Leu Lys Gln Leu Lys His Pro Asn Leu Val
109 50 55 60
110 Asn Leu Ile Glu Val Phe Arg Arg Lys Arg Lys Met His Leu Val Phe

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111 65                               70                               75                               80
112 Glu Tyr Cys Asp His Thr Leu Leu Asn Glu Leu Glu Arg Asn Pro Asn
113                               85                               90                               95
114 Gly Val Ala Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln
115                               100                               105                               110
116 Ala Leu Asn Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys
117                               115                               120                               125
118 Pro Glu Asn Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp
119                               130                               135                               140
120 Phe Gly Phe Ala Gln Ile Leu Ile Pro Gly Asp Ala Tyr Thr Asp Tyr
121 145                               150                               155                               160
122 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Val Gly Asp Thr
123                               165                               170                               175
124 Gln Tyr Gly Ser Ser Val Asp Ile Trp Ala Ile Gly Cys Val Phe Ala
125                               180                               185                               190
126 Glu Leu Leu Thr Gly Gln Pro Leu Trp Pro Gly Lys Ser Asp Val Asp
127                               195                               200                               205
128 Gln Leu Tyr Leu Ile Ile Arg Thr Leu Val Glu Thr Gly Phe Arg His
129 210                               215                               220
130 Val Asp Gln Ala Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ala
131 225                               230                               235                               240
132 Val Ala Ser Gln Ser Ala Gly Ile Thr Gly Lys Leu Ile Pro Arg His
133                               245                               250                               255
134 Gln Ser Ile Phe Lys Ser Asn Gly Phe Phe His Gly Ile Ser Ile Pro
135                               260                               265                               270
136 Glu Pro Glu Asp Met Glu Thr Leu Glu Glu Lys Phe Ser Asp Val His
137                               275                               280                               285
138 Pro Val Ala Leu Asn Phe Met Lys Gly Cys Leu Lys Met Asn Pro Asp
139 290                               295                               300
140 Asp Arg Leu Thr Cys Ser Gln Leu Leu Glu Ser Ser Tyr Phe Asp Ser
141 305                               310                               315                               320
142 Phe Gln Glu Ala Gln Ile Lys Arg Lys Ala Arg Asn Glu Gly Arg Asn
143                               325                               330                               335
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157 gatcctgttg ttaagaaaat agcactaaga gaaatacgta tgttgaagca attaaaacat 180
158 ccaaactcttg tgaacctcat cgagggtgttc aggagaaaaa ggaaaatgca tttagttttt 240
159 gaatactgtg atcatatact tttaaatgag ctggaaagaa acccaaatgg agttgctgat 300
160 ggagtgatca aaagcgtatt atggcaaaca cttcaagctc ttaatttctg tcatatacat 360
161 aactgtattc acagagatat aaaacctgaa aatattctaa taactaagca aggaataatc 420

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162 aagatttgtg acttcggggt tgcacaaatt ctgattccag gagatgccta caccgattat 480
163 gtagctacga gatggtaccg agctcctgaa cttcttgtgg gagatactca gtatggttct 540
164 tcagtcgata tatgggctat tgggttgtgtt tttgcagagc tcctgacagg ccagccactg 600
165 tggcctggaa aatcagatgt ggaccaactt tatctgataa tcagaacact aggaaaatta 660
166 atcccaagac atcaatcaat ctttaaaagt aacgggtttt tccatggcat cagtatacct 720
167 gagccagaag acatggaaac tcttgaggaa aagttctcag atgttcatcc tgtggctctg 780
168 aacttcatga aggggtgtct gaagatgaat ccagatgaca gattaacctg ttcccaactc 840
169 ctggagagct cctactttga ttcttttcaa gaggcccaa ttaaaagaaa agcacgtaat 900
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182 20 25 30
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184 35 40 45
185 Leu Arg Glu Ile Arg Met Leu Lys Gln Leu Lys His Pro Asn Leu Val
186 50 55 60
187 Asn Leu Ile Glu Val Phe Arg Arg Lys Arg Lys Met His Leu Val Phe
188 65 70 75 80
189 Glu Tyr Cys Asp His Thr Leu Leu Asn Glu Leu Glu Arg Asn Pro Asn
190 85 90 95
191 Gly Val Ala Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln
192 100 105 110
193 Ala Leu Asn Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys
194 115 120 125
195 Pro Glu Asn Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp
196 130 135 140
197 Phe Gly Phe Ala Gln Ile Leu Ile Pro Gly Asp Ala Tyr Thr Asp Tyr
198 145 150 155 160
199 Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Val Gly Asp Thr
200 165 170 175
201 Gln Tyr Gly Ser Ser Val Asp Ile Trp Ala Ile Gly Cys Val Phe Ala
202 180 185 190
203 Glu Leu Leu Thr Gly Gln Pro Leu Trp Pro Gly Lys Ser Asp Val Asp
204 195 200 205
205 Gln Leu Tyr Leu Ile Ile Arg Thr Leu Gly Lys Leu Ile Pro Arg His
206 210 215 220
207 Gln Ser Ile Phe Lys Ser Asn Gly Phe Phe His Gly Ile Ser Ile Pro
208 225 230 235 240
209 Glu Pro Glu Asp Met Glu Thr Leu Glu Glu Lys Phe Ser Asp Val His
210 245 250 255
211 Pro Val Ala Leu Asn Phe Met Lys Gly Cys Leu Lys Met Asn Pro Asp
212 260 265 270

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213 Asp Arg Leu Thr Cys Ser Gln Leu Leu Glu Ser Ser Tyr Phe Asp Ser
214          275          280          285
215 Phe Gln Glu Ala Gln Ile Lys Arg Lys Ala Arg Asn Glu Gly Arg Asn
216          290          295          300
217 Arg Arg Arg Gln Gln Val Arg Gly Cys Val Trp Leu Leu Gln Leu Cys
218 305          310          315          320
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224 <212> TYPE: DNA
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231 ccaaattcttg tgaacctcat cgaggtgttc aggagaaaaa ggaaaatgca tttagttttt      240
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249 Lys Lys Phe Val Glu Ser Glu Asp Asp Pro Val Val Lys Lys Ile Ala
250          35          40          45
251 Leu Arg Glu Ile Arg Met Leu Lys Gln Leu Lys His Pro Asn Leu Val
252          50          55          60
253 Asn Leu Ile Glu Val Phe Arg Arg Lys Arg Lys Met His Leu Val Phe
254 65          70          75          80
255 Glu Tyr Cys Asp His Thr Leu Leu Asn Glu Leu Glu Arg Asn Pro Asn
256          85          90          95
257 Gly Val Ala Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln
258          100          105          110
259 Ala Leu Asn Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys
260          115          120          125
261 Pro Glu Asn Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp
262          130          135          140
263 Phe Gly Phe Ala Gln Ile Leu Ser Trp Thr Ser Ser Phe Ser Gly Ala
264 145          150          155          160
265 Ser Leu Ile Gly Leu Ile Val Asp Leu Leu Asn Ser Phe Ser Ala Asn
266          165          170          175

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VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date